

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Docket No.: PF-0041-4 CON

Inventors: Coleman et al.

Title: POLYNUCLEOTIDES ENCODING THROMBIN RECEPTOR HOMOLOGS

Serial No.: To Be Assigned

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          9          18          27          36          45          54
5' ATG AGA AGT CAT ACC ATA ACA ATG ACG ACA ACT TCA GTC AGC AGC TGG CCT TAC
   M  R  S  H  T  I  T  M  T  T  T  S  V  S  S  W  P  Y

          63          72          81          90          99          108
TCC TCC CAC AGA ATG CGC TTT ATA ACC AAT CAT AGC GAC CAA CCG CCA CAA AAC
S  S  H  R  M  R  F  I  T  N  H  S  D  Q  P  P  Q  N

          117          126          135          144          153          162
TTC TCA GCA ACA CCA AAT GTT ACT ACC TGT CCC ATG GAT GAA AAA TTG CTA TCT
F  S  A  T  P  N  V  T  T  C  P  M  D  E  K  L  L  S

          171          180          189          198          207          216
ACT GTG TTA ACC ACA TCC TAC TCT GTT ATT TTC ATC GTG GGA CTG GTT GGG AAC
T  V  L  T  T  S  Y  S  V  I  F  I  V  G  L  V  G  N

          225          234          243          252          261          270
ATA ATC GCC CCC TAT GTA TTT CTG GGT ATT CAC CGT AAA AGA AAT TCC ATT CAA
I  I  A  P  Y  V  F  L  G  I  H  R  K  R  N  S  I  Q

          279          288          297          306          315          324
ATT TAT CTA CTT AAC GTA GCC ATT GCA GAC CTC CTA CTC ATC TTC TGC CTC CCT
I  Y  L  L  N  V  A  I  A  D  L  L  L  I  F  C  L  P

          333          342          351          360          369          378
TTC CGA ATA ATG TAT CAT ATT AAC CAA AAC AAG TGG ACA CTA GGT GTG ATT CTG
F  R  I  M  Y  H  I  N  Q  N  K  W  T  L  G  V  I  L

          387          396          405          414          423          432
TGC AAG GTT GTG GGA ACA CTG CTT TAT ATG AAC ATG TAC ATT AGC ATT ATT TTG
C  K  V  V  G  T  L  L  Y  M  N  M  Y  I  S  I  I  L

          441          450          459          468          477          486
CTT GGA TTC ATC AGT TTG GAT CGC TAT ATA AAA ATT AAT CGG TCT ATA CAG CAA
L  G  F  I  S  L  D  R  Y  I  K  I  N  R  S  I  Q  Q

          495          504          513          522          531          540
CGG AAG GCA ATA ACA ACC AAA CAA AGT ATT TAT GTC TGT TGT ATA GTA TGG ATG
R  K  A  I  T  T  K  Q  S  I  Y  V  C  C  I  V  W  M

          549          558          567          576          585          594
CTT GCT CTT GGT GGA TTC CTA ACT ATG ATT ATT TTA ACA CTT AAG AAA GGA GGG
L  A  L  G  G  F  L  T  M  I  I  L  T  L  K  K  G  G

          603          612          621          630          639          648
CAT AAT TCC ACA ATG TGT TTC CAT TAC AGA GAT AAG CAT AAC GCA AAA GGA GAA
H  N  S  T  M  C  F  H  Y  R  D  K  H  N  A  K  G  E

          657          666          675          684          693          702
GCC ATT TTT AAC TTC ATT CTT GTG GTA ATG TTC TGG CTA ATT TTC TTA CTA ATA
A  I  F  N  F  I  L  V  V  M  F  W  L  I  F  L  L  I

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FIGURE 1A

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711	720	729	738	747	756
ATC CTT TCA TAT ATT AAG ATT GGG AAG AAT CTA TTG AGG ATT TCT AAA AGG AGG					
I L S Y I K I G K N L L R I S K R R					
765	774	783	792	801	810
TCA AAA TTT CCT AAT TCT GGT AAA TAT GCC ACT ACA GCT CGT AAC TCC TTT ATT					
S K F P N S G K Y A T T A R N S F I					
819	828	837	846	855	864
GTA CTT ATC ATT TTT ACT ATA TGT GTG GGT CCC TAT CAT GCC TTT CGA TTC ATC					
V L I I F T I C V G P Y H A F R F I					
873	882	891	900	909	918
TAC ATT TCT TCA CAG CTA AAT GTA TCA TCT TGC TAC TGG AAA GAA ATT GTT CAC					
Y I S S Q L N V S S C Y W K E I V H					
927	936	945	954	963	972
AAA ACC AAT GAG ATC ATG CTG GTT CTC TCA TCT TTC AAT AGT TGG TTA GAT CCA					
K T N E I M L V L S S F N S W L D P					
981	990	999	1008	1017	1026
GTC ATG TAT TTC CTG ATG TCC AGT AAC ATT CGC AAA ATA ATG TGC CAA CTT CTT					
V M Y F L M S S N I R K I M C Q L L					
1035	1044	1053	1062	1071	1080
TTT AGA CGA TTT CAA GGT GAA CCA AGT AGG AGT GAA AGC ACT TCA GAA TTT AAA					
F R R F Q G E P S R S E S T S E F K					
1089	1098	1107	1116	1125	1134
CCA GGA TAC TCC CTG CAT GAT ACA TCT GTG GCA GGG AAA ATA CAG TCT AGT TCT					
P G Y S L H D T S V A G K I Q S S S					
1143					
GAA AGT ACT 3'					
E S T					

FIGURE 1B

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.....Q.....T.....C.....W.L.A..G.....	Consensus #1
FLAVVRSIQSLSAITLGGQAI FVCLAVWALALGGVVTLVLK	Majority
210 220 230 240	
201 FLAVVYPMQSLSWRTLGRASFTCLAIWALAIAGVVPPLVLK	thrombin R
153 YIKINRSIQQRKAITTKQSIYVCCIVWMLALGGFLTMII-	86700
..T....G..N..T..C.....G.....F.....V..F..	Consensus #1
ELTLQVGGGLNITTTCHDVLLDET LAEGEAAFFSAI LAVFFF	Majority
250 260 270 280	
241 EQTIQVPGLNITTC HDVVLNETLLEGYYAAYYFSAFSAVFF	thrombin R
192 -LTLKKGGHNSMTMCFHYRDKHNAKG E A I F N F - - I L V V M F W	86700
.....Y...I...L.....R...K.....A..	Consensus #1
VILLIIIVSVSIGKNLLSSAVANRSSKFPSSGLFASAA R	Majority
290 300 310 320	
281 VPLIISTVCYVSIIRCLSSSAVANRSKK--SRALFLSAA-	thrombin R
229 LIFLLIISLYIKIGKNLLR--ISKRRSKFPNSGKYATTAR	86700
....V...IF..IC.GP.....S.....Y...	Consensus #1
NSFIVLIIFIICVGPNTALLIAHFIFLSSTLTVSAA YFAE	Majority
330 340 350 360	
318 - - - - VFCIFIFIICFGPTNVLLIAHYSFLSHTSTTEAA YFAY	thrombin R
267 NSFIVLIIIFITICVGPYHAF--RFIYISQLNVSSCCYWK E	86700
.....SS...S...DP...Y...SS.....L..	Consensus #1
L VHKTNEIMVSVSSISSWLDPPVIYFFLASSEIQKIVYSLLF	Majority
370 380 390 400	
354 LLC - - - - VCVSSISSCIDPPLIYYAASS ECQRYYVYSI LC	thrombin R
304 IVHKTNEIMLVLLSSFNSSWLDPPVMYFLMSSNIRKIMCQL LF	86700

FIGURE 2B

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Consensus #1
Majority

thrombin R
86700

. P S S S T
 R K E S G D P S S S E S S G E L K A G K S L T D S S V A G N I I S S S L L T
 410 420 430
 388 C K E S S D P S S Y N S S G Q L M A S K M D T C S S N L N N S I Y K K L L T
 344 R R F Q G E P S R S E S T S E F K P G Y S L H D T S V A G K I Q S S S E S T

FIGURE 2C